Appendix: Abstract of Southern *et al.*, reference 7 in cited reference Pease *et al.*

Analyzing and Comparing Nucleic Acid Sequences by Hybridization to Arrays of Oligonucleotides: Evaluation Using Experimental Models.

Southern EM, Maskos U, Elder JK
Department of Biochemistry, University of Oxford, United Kingdom
Genomics **13**(4):1008-17 (Aug 1992)

An efficient method was developed for making **complete sets** of oligonucleotides of defined length, covalently attached to the surface of a glass plate, by synthesizing them in situ. A device carrying **all octapurine sequences** was used to explore factors affecting molecular hybridization of the tethered oligonucleotides, to develop computer-aided methods for analyzing the data, and to test the feasibility of using the method for sequence analysis. Further development is needed before the method can be used routinely, but our work shows that it has a number of potential advantages over gel-based methods: it should be easy to automate; the quality of the sequence results can be evaluated statistically; it provides a powerful way of comparing related sequences and detecting mutation; it can be applied to both DNA and RNA; and specific motifs can be incorporated into all sequences of the array to focus analysis on sequences of biological interest.
[emphasis added]